```
   1 CCGCCCTCCC CCGGCCGAGC TCCAGGGCTG CCGCCTAGCA GCTCCCGGCG
  51 GGAGAGCGGT TCAGAGCTCG CTCCCACCCC TTCCCGGCGT GATTGATCCG
 101 TCACGGGCGC CTCCGCTGCC GCCGCCGCCG CCGCGGCCGT TCTGAGCCGA
 151 GCCGGAACCC TAGCCCGAGA CGGAGCCGGG GCCCGGGCCG GCGCCATTGC
 201 GCGGGCGCCG CGGGAAGACC TTGGCGCGGG GCGGCGGGCC GGGCCAGGCC
 251 ATGCGGGCCG AGTGAGCCGG CGCCCGCAGC CCGCGGCGCG GCATGGCTTC
 301 CCCGCGGAGC TCCGGGCAGC CCGGGCCGCC GCCGCCGCCG CCACCGCCGC
 351 CCGCGCGCCT GCTACTGCTA CTGCTGCTGC CGCTGCTGCT GCCTCTGGCG
 401 CCCGGGGCCT GGGGCTGGGC GCGGGGCGCC CCCCGGCCGC CGCCCAGCAG
 451 CCCGCCGCTC TCCATCATGG GCCTCATGCC GCTCACCAAG GAGGTGGCCA
 501 AGGGCAGCAT CGGGCGCGGT GTGCTCCCCG CCGTGGAACT GGCCATCGAG
 551 CAGATCCGCA ACGAGTCACT CCTGCGCCCC TACTTCCTCG ACCTGCGGCT
 601 CTATGACACG GAGTGCGACA ACGCAAAAGG GTTGAAAGCC TTCTACGATG
 651 CAATAAAATA CGGGCCGAAC CACTTGATGG TGTTTGGAGG CGTCTGTCCA
 701 TCCGTCACAT CCATCATTGC AGAGTCCCTC CAAGGCTGGA ATCTGGTGCA
 751 GCTTTCTTTT GCTGCAACCA CGCCTGTTCT AGCCGATAAG AAAAAATACC
 801 CTTATTTCTT TCGGACCGTC CCATCAGACA ATGCGGTGAA TCCAGCCATT
 851 CTGAAGTTGC TCAAGCACTA CCAGTGGAAG CGCGTGGGCA CGCTGACGCA
 901 AGACGTTCAG AGGTTCTCTG AGGTGCGGAA TGACCTGACT GGAGTTCTGT
 951 ATGGCGAGGA CATTGAGATT TCAGACACCG AGAGCTTCTC CAACGATCCC
1001 TGTACCAGTG TCAAAAAGCT GAAGGGGAAT GATGTGCGGA TCATCCTTGG
1051 CCAGTTTGAC CAGAATATGG CAGCAAAAGT GTTCTGTTGT GCATACGAGG
1101 AGAACATGTA TGGTAGTAAA TATCAGTGGA TCATTCCGGG CTGGTACGAG
1151 CCTTCTTGGT GGGAGCAGGT GCACACGGAA GCCAACTCAT CCCGCTGCCT
1201 CCGGAAGAAT CTGCTTGCTG CCATGGAGGG CTACATTGGC GTGGATTTCG
1251 AGCCCCTGAG CTCCAAGCAG ATCAAGACCA TCTCAGGAAA GACTCCACAG
1301 CAGTATGAGA GAGAGTACAA CAACAAGCGG TCAGGCGTGG GGCCCAGCAA
1351 GTTCCACGGG TACGCCTACG ATGGCATCTG GGTCATCGCC AAGACACTGC
1401 AGAGGGCCAT GGAGACACTG CATGCCAGCA GCCGGCACCA GCGGATCCAG
1451 GACTTCAACT ACACGGACCA CACGCTGGGC AGGATCATCC TCAATGCCAT
1501 GAACGAGACC AACTTCTTCG GGGTCACGGG TCAAGTTGTA TTCCGGAATG
1551 GGGAGAGAAT GGGGACCATT AAATTTACTC AATTTCAAGA CAGCAGGGAG
1601 GTGAAGGTGG GAGAGTACAA CGCTGTGGCC GACACACTGG AGATCATCAA
1651 TGACACCATC AGGTTCCAAG GATCCGAACC ACCAAAAGAC AAGACCATCA
1701 TCCTGGAGCA GCTGCGGAAG ATCTCCCTAC CTCTCTACAG CATCCTCTCT
1751 GCCCTCACCA TCCTCGGGAT GATCATGGCC AGTGCTTTTC TCTTCTTCAA
1801 CATCAAGAAC CGGAATCAGA AGCTCATAAA GATGTCGAGT CCATACATGA
1851 ACAACCTTAT CATCCTTGGA GGGATGCTCT CCTATGCTTC CATATTTCTC
1901 TTTGGCCTTG ATGGATCCTT TGTCTCTGAA AAGACCTTTG AAACACTTTG
1951 CACCGTCAGG ACCTGGATTC TCACCGTGGG CTACACGACC GCTTTTGGGG
2001 CCATGTTTGC AAAGACCTGG AGAGTCCACG CCATCTTCAA AAATGTGAAA
2051 ATGAAGAAGA AGATCATCAA GGACCAGAAA CTGCTTGTGA TCGTGGGGGG
2101 CATGCTGCTG ATCGACCTGT GTATCCTGAT CTGCTGGCAG GCTGTGGACC
2151 CCCTGCGAAG GACAGTGGAG AAGTACAGCA TGGAGCCGGA CCCAGCAGGA
```

FIG.1A

```
2201 CGGGATATCT CCATCCGCCC TCTCCTGGAG CACTGTGAGA ACACCCATAT
2251 GACCATCTGG CTTGGCATCG TCTATGCCTA CAAGGGACTT CTCATGTTGT
2301 TCGGTTGTTT CTTAGCTTGG GAGACCCGCA ACGTCAGCAT CCCCGCACTC
2351 AACGACAGCA AGTACATCGG GATGAGTGTC TACAACGTGG GGATCATGTG
2401 CATCATCGGG GCCGCTGTCT CCTTCCTGAC CCGGGACCAG CCCAATGTGC
2451 AGTTCTGCAT CGTGGCTCTG GTCATCATCT TCTGCAGCAC CATCACCCTC
2501 TGCCTGGTAT TCGTGCCGAA GCTCATCACC CTGAGAACAA ACCCAGATGC
2551 AGCAACGCAG AACAGGCGAT TCCAGTTCAC TCAGAATCAG AAGAAAGAAG
2601 ATTCTAAAAC GTCCACCTCG GTCACCAGTG TGAACCAAGC CAGCACATCC
2651 CGCCTGGAGG GCCTACAGTC AGAAAACCAT CGCCTGCGAA TGAAGATCAC
2701 AGAGCTGGAT AAAGACTTGG AAGAGGTCAC CATGCAGCTG CAGGACACAC
2751 CAGAAAAGAC CACCTACATT AAACAGAACC ACTACCAAGA GCTCAATGAC
2801 ATCCTCAACC TGGGAAACTT CACTGAGAGC ACAGATGGAG GAAAGGCCAT
2851 TTTAAAAAAT CACCTCGATC AAAATCCCCA GCTACAGTGG AACACAACAG
2901 AGCCCTCTCG AACATGCAAA GATCCTATAG AAGATATAAA CTCTCCAGAA
2951 CACATCCAGC GTCGGCTGTC CCTCCAGCTC CCCATCCTCC ACCACGCCTA
3001 CCTCCCATCC ATCGGAGGCG TGGACGCCAG CTGTGTCAGC CCCTGCGTCA
3051 GCCCCACCGC CAGCCCCCGC CACAGACATG TGCCACCCTC CTTCCGAGTC
3101 ATGGTCTCGG GCCTGTAAGG GTGGGGGGCC TGGGCCCGGG GCCTCCCCCG
3151 TGACAGAACC ACACTGGGCA GAGGGGTCTG CTGCAGAAAC ACTGTCGGCT
3201 CTGGCTGCGG AGAAGCTGGG CACCATGGCT GGCCTCTCAG GACCACTCGG
3251 ATGGCACTCA GGTGGACAGG ACGGGGCAGG GGGAGACTTG GCACCTGACC
3301 TCGAGCCTTA TTTGTGAAGT CCTTATTTCT TCACAAAGAA GAGGAACGGA
3351 AATGGGACGT CTTCCTTAAC ATCTGCAAAC AAGGAGGCGC TGGGATATCR
3401 AATTCCACCA CACTGGCGGC CCGCGCTTGS TCSTAATCAT GGTCATAACT
3451 GTTTCCTGTG TTGAAATTGT TATCCGCTCC
```

FIG. 1B

```
  1 MASPRSSGQP GPPPPPPPPP ARLLLLLLLP LLLPLAPGAW GWARGAPRPP
 51 PSSPPLSIMG LMPLTKEVAK GSIGRGVLPA VELAIEQIRN ESLLRPYFLD
101 LRLYDTECDN AKGLKAFYDA IKYGPNHLMV FGGVCPSVTS IIAESLQGWN
151 LVQLSFAATT PVLADKKKYP YFFRTVPSDN AVNPAILKLL KHYQWKRVGT
201 LTQDVQRFSE VRNDLTGVLY GEDIEISDTE SFSNDPCTSV KKLKGNDVRI
251 ILGQFDQNMA AKVFCCAYEE NMYGSKYQWI IPGWYEPSWW EQVHTEANSS
301 RCLRKNLLAA MEGYIGVDFE PLSSKQIKTI SGKTPQQYER EYNNKRSGVG
351 PSKFHGYAYD GIWVIAKTLQ RAMETLHASS RHQRIQDFNY TDHTLGRIIL
401 NAMNETNFFG VTGQVVFRNG ERMGTIKFTQ FQDSREVKVG EYNAVADTLE
451 IINDTIRFQG SEPPKDKTII LEQLRKISLP LYSILSALTI LGMIMASAFL
501 FFNIKNRNQK LIKMSSPYMN NLIILGGMLS YASIFLFGLD GSFVSEKTFE
551 TLCTVRTWIL TVGYTTAFGA MFAKTWRVHA IFKNVKMKKK IIKDQKLLVI
601 VGGMLLIDLC ILICWQAVDP LRRTVEKYSM EPDPAGRDIS IRPLLEHCEN
651 THMTIWLGIV YAYKGLLMLF GCFLAWETRN VSIPALNDSK YIGMSVYNVG
701 IMCIIGAAVS FLTRDQPNVQ FCIVALVIIF CSTITLCLVF VPKLITLRTN
751 PDAATQNRRF QFTQNQKKED SKTSTSVTSV NQASTSRLEG LQSENHRLRM
801 KITELDKDLE EVTMQLQDTP EKTTYIKQNH YQELNDILNL GNFTESTDGG
851 KAILKNHLDQ NPQLQWNTTE PSRTCKDPIE DINSPEHIQR RLSLQLPILH
901 HAYLPSIGGV DASCVSPCVS PTASPRHRHV PPSFRVMVSG L
```

FIG.2

Sequence: LPLLLPLAPGAWG-WARGAPRPPPSSPPLSIMGLMPLTKEVAKGSIGRGVLPAVELAIEQIRNE
|(signal) |(mature peptide)
29 42

Other entries above 3.50

Score 11.1 at residue 39

Sequence: LLLLPLLLPLAPG-AWGWARGAPRPPPSSPPLSIMGLMPLTKEVAKGSIGRGVLPAVELAIEQI
|(signal) |(mature peptide)
26 39
Score 8.6 at residue 38

Sequence: LLLLLPLLLPLAP-GAWGWARGAPRPPPSSPPLSIMGLMPLTKEVAKGSIGRGVLPAVELAIEQ
|(signal) | (mature peptide)
25 38
Score 8.1 at residue 35

Sequence: RLILLLLLPLLLP-LAPGAWGWARGAPRPPPSSPPLSIMGLMPLTKEVAKGSIGRGVLPAVELA
|(signal) |(mature peptide)
22 35
Score 7.9 at residue 36

Sequence: LILLLLLPLLLPL-APGAWGWARGAPRPPPSSPPLSIMGLMPLTKEVAKGSIGRGVLPAVELAI
|(signal) |(mature peptide)
23 36
Score 6.2 at residue 9

Sequence: -QPGRPPPPPPPPARLILLLLLPLLLPLAPGAWGWARGAPRPPPSSPPLSI
|(signal) |(mature peptide)
-4 9
Score 5.7 at residue 46

Sequence: LPLAPGAWGWARG-APRPPPSSPPLSIMGLMPLTKEVAKGSIGRGVLPAVELAIEQIRNESLLR
|(signal) |(mature peptide)
33 46
Score 5.6 at residue 747

Sequence: ITLCLVFVPKLIT-LRTNPDAATQNRRFQFTQNQKKEDSKTSTSVTSVNQASTSRLEGLQSENH
|(signal) |(mature peptide)
734 747
Score 5.0 at residue 44

Sequence LLLPLAPGAWGWA-RGAPRPPPSSPPLSIMGLMPLTKEVAKGSIGRGVLPAVELAIEQIRNESL
|(signal) |(mature peptide)
31 44
Score 4.9 at residue 497

FIG.3A

Sequence: ILSALTILGMIMA-SAFLFFNIKNRNQKLIKMSSPMNNLIILGGMLSYASIFLFGLDGSFVSE
|(signal) |(mature peptide)
484 497
Score 4.5 at residue 141

Sequence: LMVFGGVCPSVTS-IIAESLQGWNLVQLSFAATTPVLADKKKYPYFFRTVPSDNAVNPAILKLL
|(signal) |(mature peptide)
128 141
Score 4.4 at residue 734

Sequence: FCIVALVIIFCST-ITLCLVFVPKLITLRTNPDAATQNRRFQFTQNQKKEDSKTSTSVTSVNQA
|(signal) |(mature peptide)
721 734
Score 4.1 at residue 165

Sequence: VQLSFAATTPVLA-DKKKYPYFFRTVPSDNAVNPAILKLLKHYQWKRVGTLTQDVQRFSEVRND
|(signal) |(mature peptide)
152 165
Score 3.6 at residue 158

Sequence: SLQGWNLVQLSFA-ATTPVLADKKKYPYFFRTVPSDNAVNPAILKLLKHYQWKRVGTLTQDVQR
|(signal) |(mature peptide)
145 158

FIG.3B

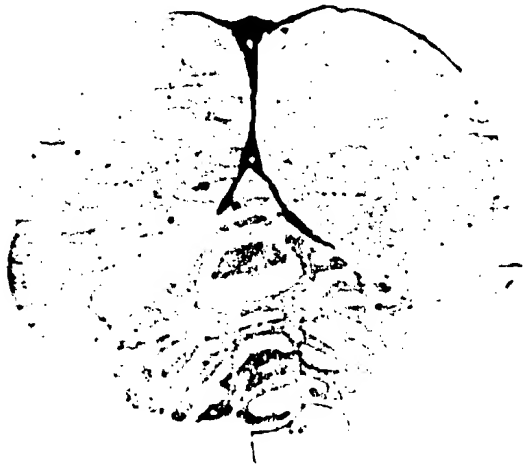
Distribution of mRNA for EST z43654 in squirrel monkey brain.

at level of caudate and putamen

at level of thalamus and hippocampus

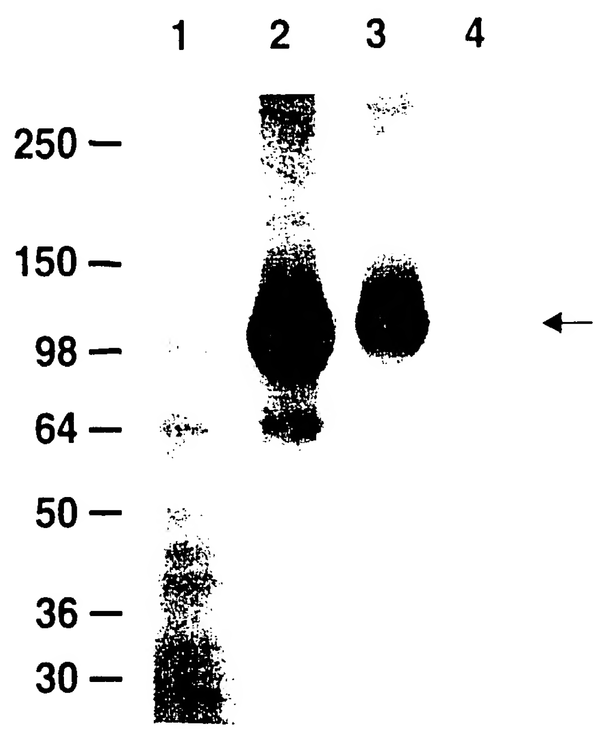
FIG.4

at level of cerebellum and occipital cortex



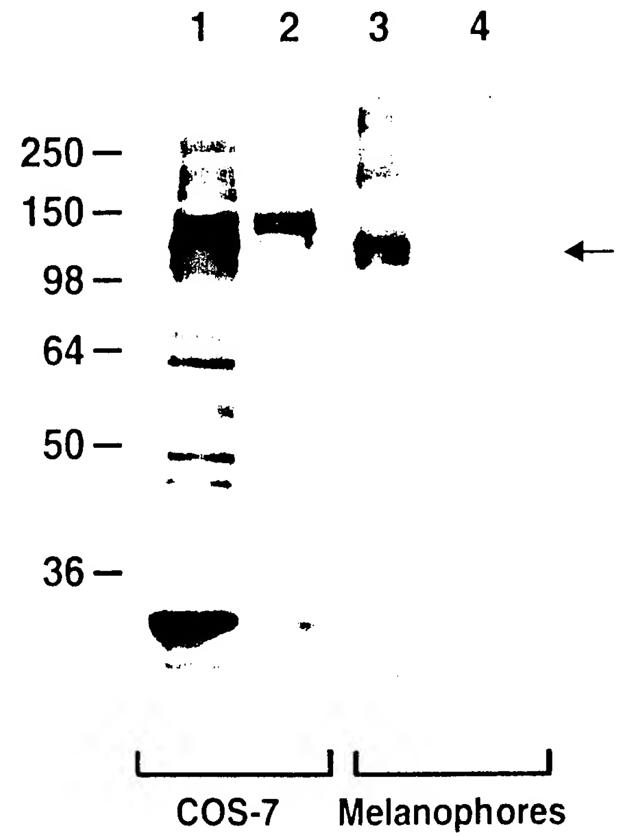
example of cold displayed

APPROVED BY DRAFTSMAN	O.G. FIG.	
	CLASS	SUBCLASS



1- HG20/PCR 3.1
2- FLAG-HG20/pcDNA 3:1
3- Mouse $GABA_B$/ pcDNA 3:1
4- pcDNA 3:1

FIG.5A



1- FLAG-HG20/pcDNA 3.1
2- pcDNA 3.1
3- FLAG-HG20/pcDNA 3.1
4- pcDNA 3.1

FIG.5B

```
PLTKEVAK-GSIGR-GVLPAVELAIEQIRNESLLRPYFLDLRLYDTECDNAKGLKAFYDA
:.:  ::. :.. : :.:    .X:::: . . .    :.  .::  :X  ... .  .
PVTGPVAQYGDMQRAGAL----MAIEQINKAGGVNGAQLEGVIYDDACDPKQAVAVANKV

IKYGPNHLMVFGGVCPSVTSIIAESLQGWNLVQLSFAATTPVLADKKKYPYFFRTVPSDN
.. : .  .: : :: : :. .. . ..... .::.: .. .. :  .:::.  ::
VNDGVK--FVVGHVCSSSTQPATDIYEDEGVLMITPSATAPEIT-SRGYKLIFRTIGLDN

AVNPAILKLL-KHYQWKRVGTLTQDVQRFSE-VRNDLTGVLYGEDIEISDTESFS---ND
  .:.  :.. ..:. : ...: .: :...: . ...  ..    :...  :...   .:
MQGPVAGKFIAERYKVKTIAVL-HDKQQYGEGIATEVKKTVEDAGIRVAVFEGLNAGDKD

PCTSVKKLKGNDVRII-LGQFDQNM
  . ..:::   :... .: .  .:
FNALISKLKKAGVQFVYFGGYHPEM
```

FIG.6

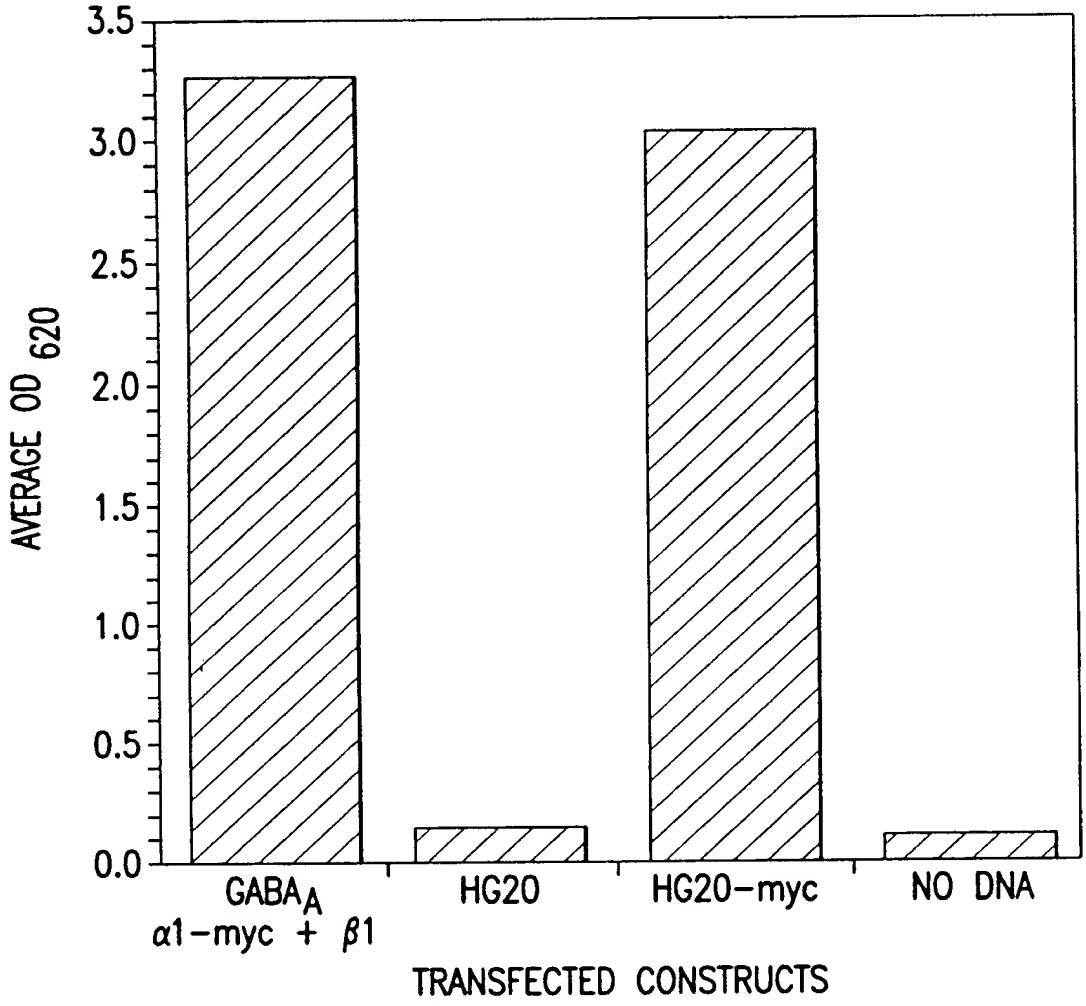


FIG.7

```
GABA-BR1b  MGPGGPCTPVGWPLPLLLVMAAGVAPVWASHSPHL---PRPHPRVPPHPSSERRAVYIGALFPMSGGWP-G--GQ  69
HG20       MASPRSSGQPGRPPPPPPPPARLILLLLLPLLLPLAPGAWGWARGAPRPPPSSPPLSIMGLMPLTKEVAKGSIGR  75
Consensus  M.........G.P.P.....A.............L........R..P.P........I..L.P.......G..G.  75

GABA-BR1b  ACQPAVEMALEDVNSRRDILPDYELKLIHHDSKCDPGQATKYLYELLYNDPIKIILMPG-CSSVSTLVAEAARMW  143
HG20       GVLPAVELAIEQIRN-ESLLRPYFLDLRLYDTECDNAKGLKAFYDAIKYGPNHLMVFGGVCPSVTSIIAESLQGW  149
Consensus  ...PAVE.A.E........L..Y.L.L...D..CD.....K..Y......P.......G.C.SV....AE....W  150

GABA-BR1b  NLIVLSYGSSSPALSNRQRFPTFFRTHPSATLHNPTRVKLFEKWGWKKIATIQQTTEVFTSTLDDLEERVKEAGI  218
HG20       NLVQLSFAATTPVLADKKKYPYFFRTVPSDNAVNPAILKLLKHYQWKRVGTLTQDVQRFSEVRNDLTGVLYGEDI  224
Consensus  NL..LS.....P.L......P.FFRT.PS....NP...KL.....WK...T..Q....F.....DL........I  225

GABA-BR1b  EITFRQSFFSDPAVPVKNLKRQDARIIVGLFYETEARKVFCEVYKERLFGKKYVWFLIGWYADNWF---KTYDPS  290
HG20       EISDTESFSNDPCTSVKKLKGNDVRIILGQFDQNMAAKVFCCAYEENMYGSKYQWIIPGWYEPSWWEQVHTEANS  299
Consensus  EI....SF..DP...VK.LK...D.RII.G.F...A.KVFC..Y.E...G.KY.W...GWY...W.....T...S  300

GABA-BR1b  INCTVEEMTEAVEGHITTEIVMLNPANTRSISNMTSQEFVEKLTKRLKRHPEETGGFQEAPLAYDAIWALALALN  365
HG20       SRCLRKNLLAAMEGYIGVDFEPLSSKQIKTISGKTPQQY-EREYNN-KRSGVGPSKFHGYAYDGIWVIAKTLQRA  372
Consensus  ..C.......A.EG.I......L.......IS..T.Q...E......KR.......F...........A..L...  375

GABA-3R1b  KTSGGGGRSGVRLEDFNYNNQTITDQIYRAMNSSSFEGVSGHVVFDASGSRMAWTLIEQLQGGSYKKIGYYDSTK  440
HG20       METLHASSRHQRIQDFNYTDHTLGRIILNAMNETNFFGVTGQVVFR-NGERMGTIKFTQFQDSREVKVGEYNAVA  446
Consensus  ..........R..DFNY...T...I....AMN..F.GV.G.VVF...G.RM......Q.Q.....K.G.Y....  450

GABA-BR1b  DDLSWSKTDKWIGGSPPADQTLVIKTFRFLSQKLFISVSVLSSLGIVLAVVC---LSFNIYNSHVRYIQNSQPNL  512
HG20       DTLEIINDTIRFQGSEPPKDKTII--LEQLRKISLPLYSILSALTILGMIMASAFLFFNIKNRNQKLIKMSSPYM  519
Consensus  D.L..........GS.P......I.....L........S.LS.L.I.........L.FNI.N.....I..S.P..  525
```

FIG.8A

```
GABA-BR1b NNLTAVGCSLALAAVFPLGLDGYHIGRSQFPFVCQARLWLLGLGFSLGYGSMFTKIWWVHTVFTKKEEKKEWRKT   587
HG20      NNLIILGGMLSYASIFLFGLDGSFVSEKTFETLCTVRTWILTVGYTTAFGAMFAKTWRVHAIF--KNVKMK-KKI   591
Consensus NNL...G..L..A..F..GLDG.......F...C..R.W.L..G.....G.MF.K.W.VH..F..K..K....K.   600

GABA-BR1b LEPWKLYATVGLLVGMDVLTLAIWQIVDPLHRTIETFAKEEPKEDIDVSILPQLEHCSSKKMNTWLGIFYGYKGL   662
HG20      IKDQKLLVIVGGMLLIDLCILICWQAVDPLRRTVEKYSMEPDPAGRDISIRPLLEHCENTHMTIWLGIVYAYKGL   666
Consensus ....KL...VG.....D...L..WQ.VDPL.RT.E....E......D.SI.P.LEHC....M..WLGI.Y.YKGL   675

GABA-BR1b LLLLGIFLAYETKSVSTEKINDHRAVGMAIYNVAVLCLITAPVTMILSSQQDAAFAFASLAIVFSSYITLVVLFV   737
HG20      LMLFGCFLAWETRNVSIPALNDSKYIGMSVYNVGIMCIIGAAVSFLTRDQPNVQFCIVALVIIFCSTITLCLVFV   741
Consensus L.L.G.FLA.ET..VS....ND....GM..YNV...C.I.A.V......Q....F....L.I.F.S.ITL...FV   750

GABA-BR1b PKMRRLITRGE------W----QSETQDTMKTGSS-TNNNEEEKSRL--LEKE----------NRELEKI----   784
HG20      PKLITLRTNPDAATQNRRFQFTQNQKKEDSKTSTSVTSVNQASTSRLEGLQSENHRLRMKITELDKDLEEVTMQL   816
Consensus PK...L.T.............Q.......KT..S.T..N....SRL..L..E .............LE......   825

GABA-BR1b --IAEKE--------ERVSE----------------LRHQLQSRQQLRSRRHPPTPP--DPSGG----------   820
HG20      QDTPEKTTYIKQNHYQELNDILNLGNFTESTDGGKAILKNHLDQNPQLQWNTTEPSRTCKDPIEDINSPEHIQRR   891
Consensus ....EK.................................L...L....QL......P.....DP.............   900

GABA-BR1b -----------LPR-GPSEPPDRLSC----DGSRVHLL---YK------                            844
HG20      LSLQLPILHHAYLPSIGGVDASCVSPCVSPTASPRHRHVPPSFRVMVSGL                            941
Consensus ............LP..G.........C.......R..............                            950
```

FIG.8B

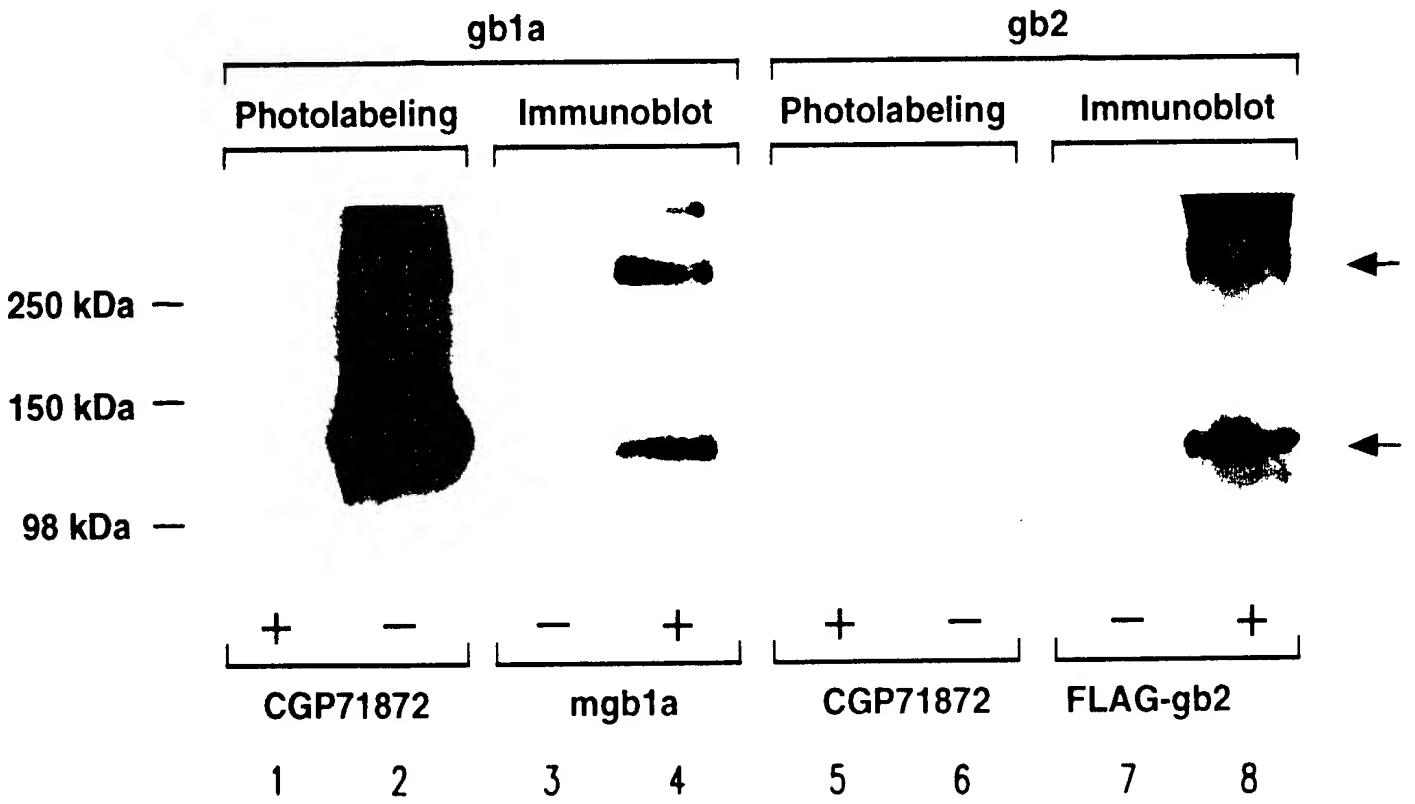


FIG.9

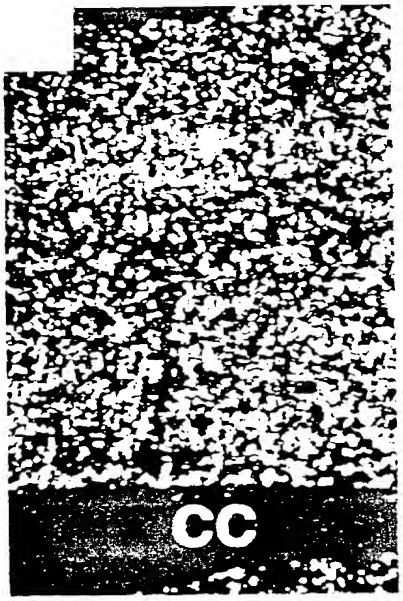


FIG.10A

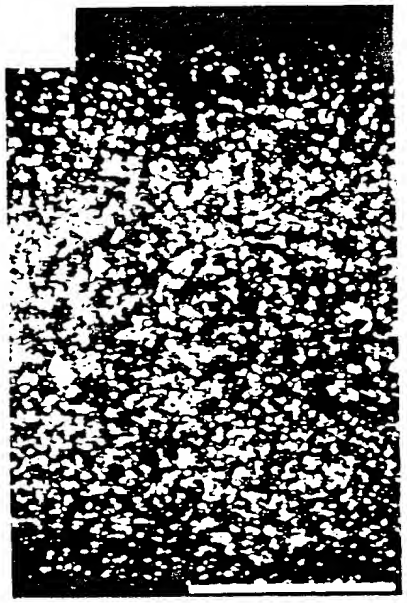


FIG.10B

FIG.10C

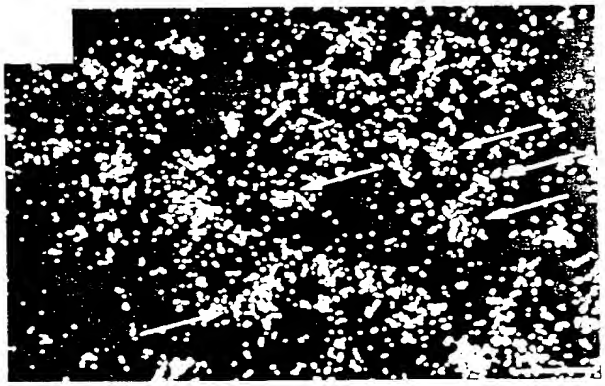


FIG.10D

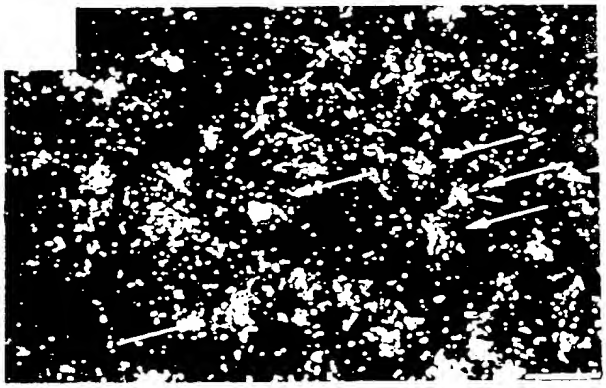


FIG.10E

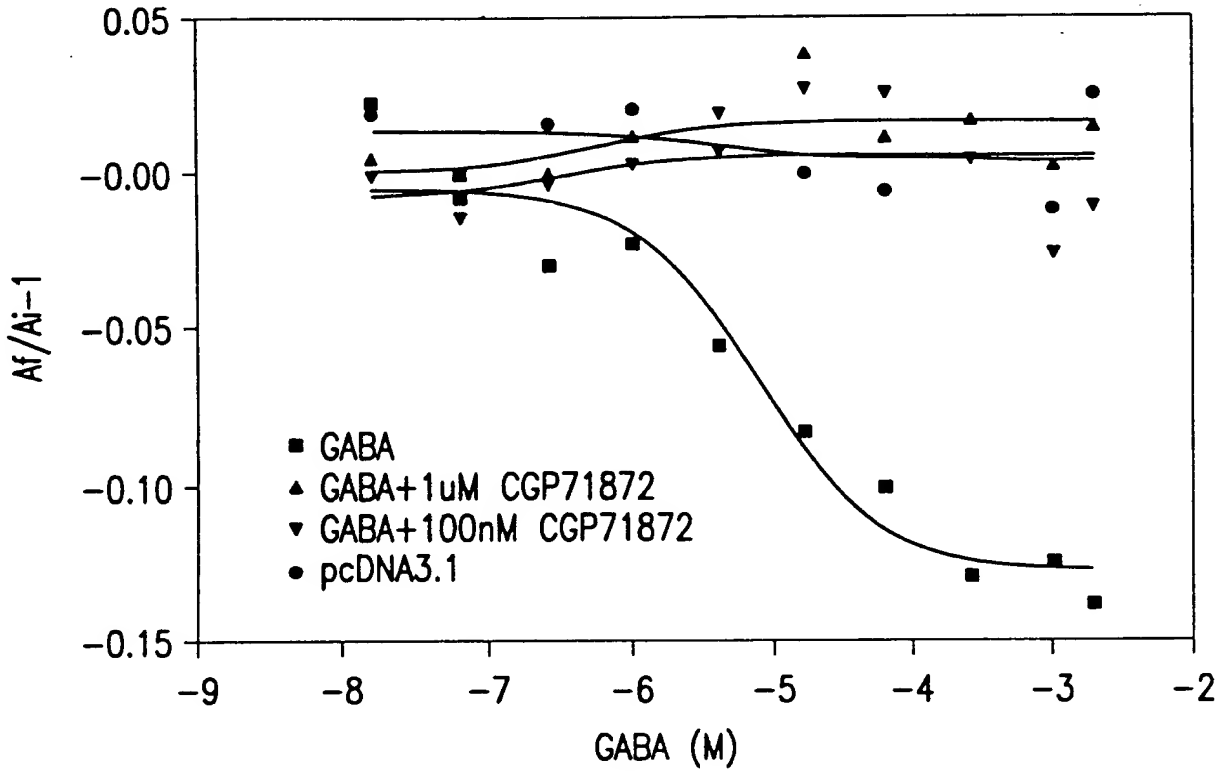


FIG. 11A

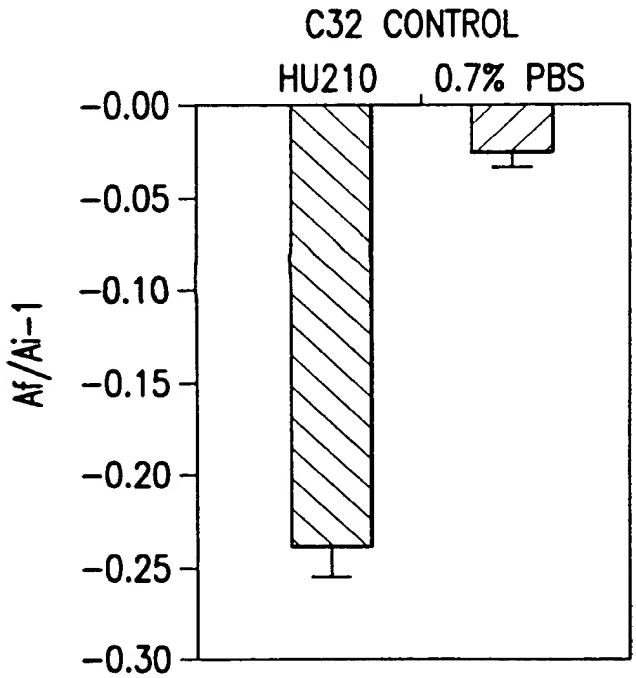


FIG. 11B

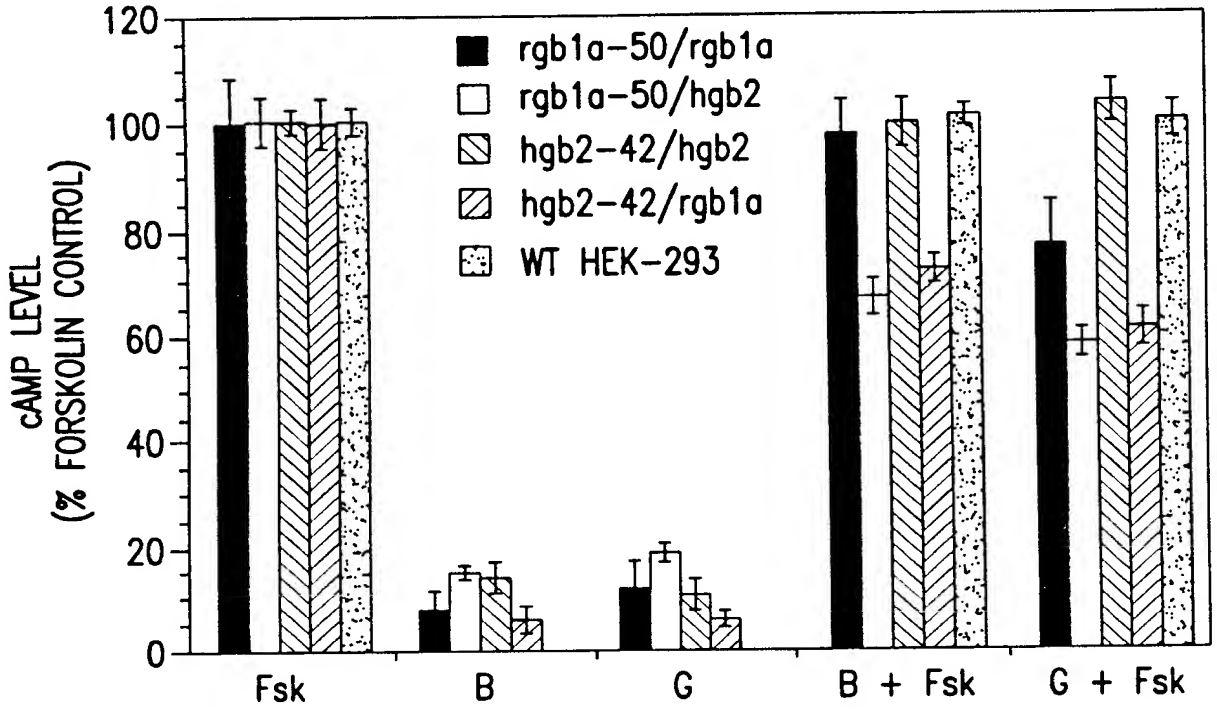


FIG. 12

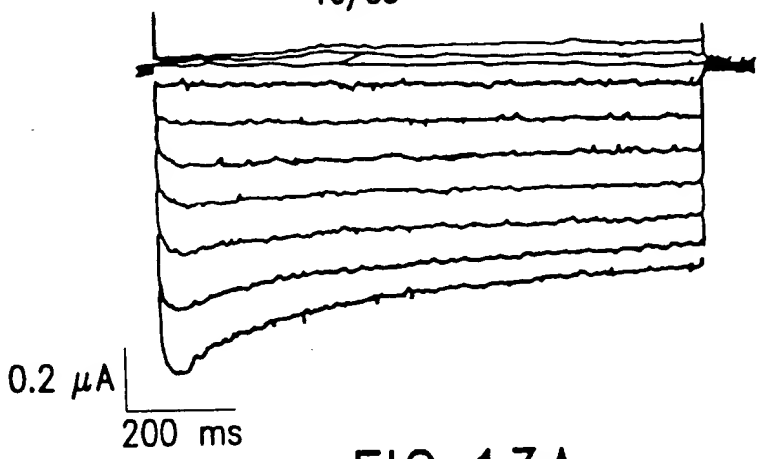


FIG. 13A

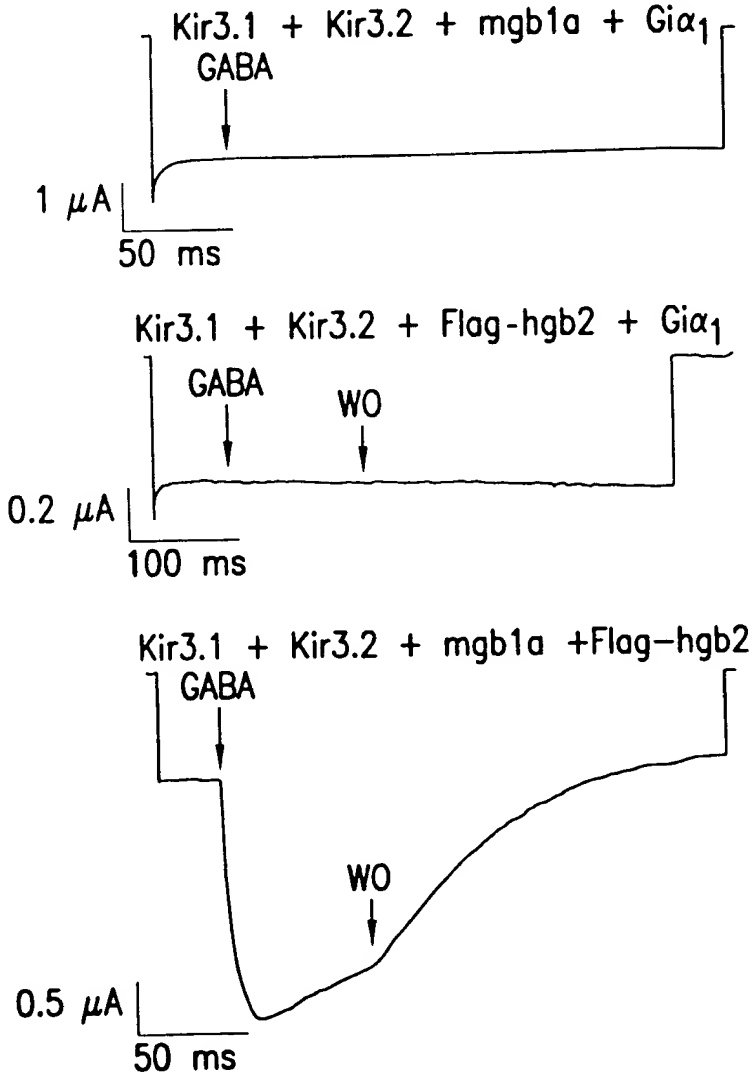


FIG. 13B

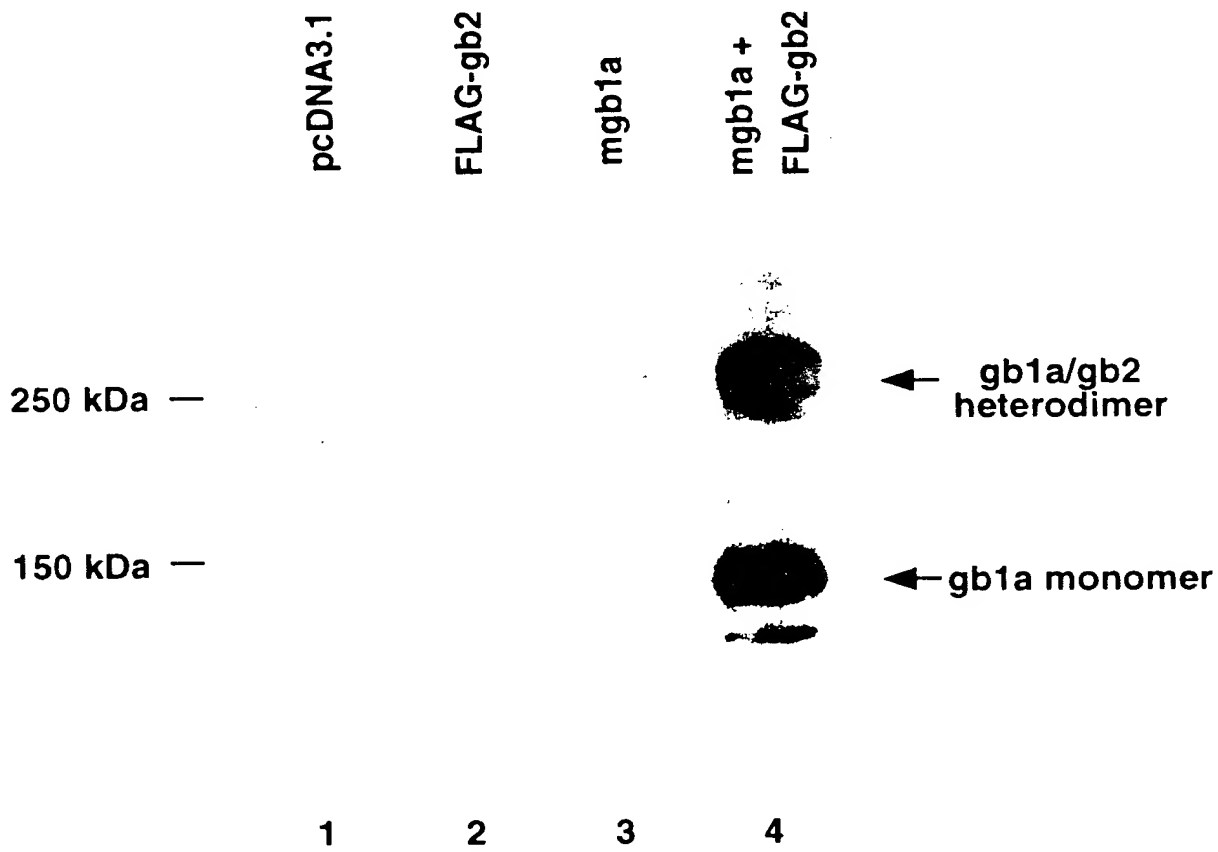


FIG.14

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   1 atgctgctgc tgctgcttct gcttctcttc ctccgccccc tgggcgctgg cggggctcag
  61 acccccaacg tcacctcgga aggttgccag attatacatc cgccctggga aggtggcatc
 121 aggtaccgtg gcttgattcg cgaccaggtg aaggccatca atttcctgcc tgtggactat
 181 gagattgaat atgtgtgccg gggcgaacgc gaggtggtgg ggcccaaggt gcgcaagtgc
 241 ctggccaacg gctcctggac ggatatggac acacccagtc gctgtgtccg aatctgctcc
 301 aagtcttatt tgaccctgga aaatgggaag gttttcctga cgggtgggga cctcccagct
 361 ctggatggag cccgggtgga tttccgatgt gaccctgact tccatctggt gggcagctcc
 421 cggagcatct gtagtcaggg ccagtggagc acccccaagc cccactgcca ggtgaatcga
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 661 ccagggcaag ccaccaagta cttgtatgaa ctactctaca acgaccccat caagatcatc
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 961 acactggatg acctggagga gcgagtgaaa gaggctggga ttgagatcac ttttcgacag
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1381 ggaggcttcc aggaggcacc actggcctat gatgctattt gggccttggc tttggccttg
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1501 aaccagacca ttacagacca aatctaccgg gccatgaact cctcctcctt tgagggtgtt
1561 tctggccacg tggtctttga tgccagcggc tcccggatgg catggacgct tatcgagcag
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1681 tggtccaaaa cagacaagtg gatcggaggg tctcccccag ccgaccagac cttggtcatc
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1801 ggcattgttc ttgctgttgt ctgtctgtcc tttaacatct acaactccca cgctcgttat
1861 atccagaatt cccagcccaa cctgaacaat ctgactgctg tgggctgctc actggcactg
1921 gctgttgtct tccctctcgg gctggatggt taccacatag ggagaagcca gttcccgttt
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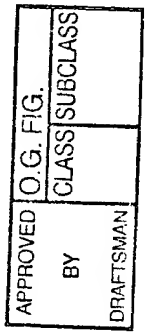
FIG.15



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HITTEIVMLNPANTRSISNMTSQEFVEKLTKRLKRHPEETGGFQEAPLAYDAIWALALAL
NKTSGGGGRSGVRLEDFNYNNQTITDQIYRAMNSSSFEGVSGHVVFDASGSRMAWTLIEQ
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GIVLAVVCLSFNIYNSHARYIQNSQPNLNNLTAVGCSLALAVVFPLGLDGYHIGRSQFPF
VCQARLWLLGLGFSLGYGSMFTKIWWVHTVFTKKEEKKEWRKTLEPWKLYATVGLLVGMD
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FIG.16

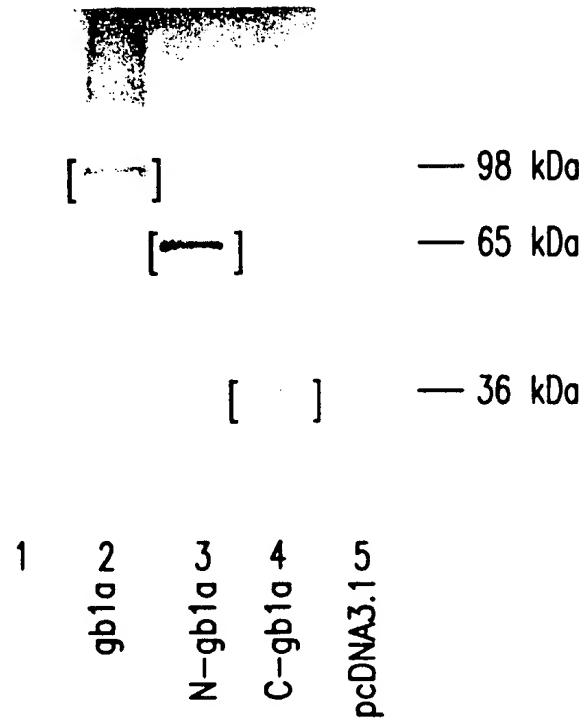

FIG.17A

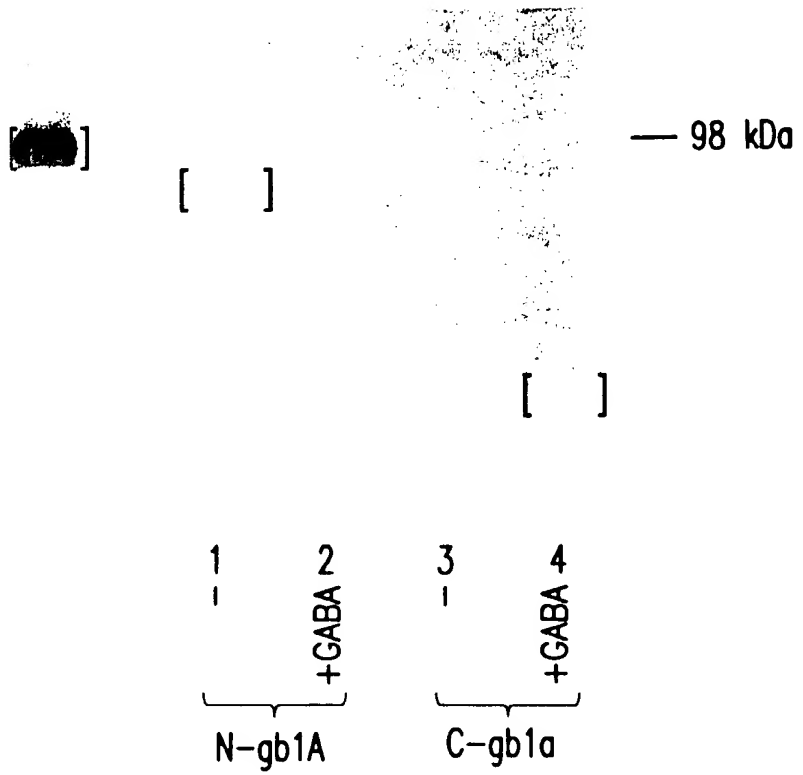

FIG.17B

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KSYLTLENGKVFLTGGDLPALDGARADFRCDPDFHLVGSSRSICSQGQWST
PKPHCQVNRTPHSERRAVYIGALFPMSGGWPGGQACQPAVEMALEDVNS
RRDILPDYELKLIHHDSKCDPGQATKYLYELLYNDPIKIILMPGCSSVSTLV
AEAARMWNLIVLSYGSSSPALSNRQRFPTFFRTHPSATLHNPTRVKLFEKW
GWKKIATIQQTTEVFTSTLDDLEERVKEAGIEITFRQSFFSDPAVPVKNLKRQ
DARIIVGLFYETEARKVFCEVYKERLFGKKYVWFLIGWYADNWFKIYDPS
INCTVDEMTEAVEGHITTEIVMLNPANTRSISNMTSQEFVEKLTKRLKRHPE
ETGGFQEAPLAYDAIWALALALNKTSGGGGRSGVRLEDFNYNNQTITDQI
YRAMNSSSFEGVSGHVVFDASGSRMAWTLIEQLQGGSYKKIGYYDSTKDD
LSWSKTDKWIGGSPPADQTLVIKTFRFLSQKLFISVSVLSSLGIVLAVVCLSF
NIYNSHVRYIQNSQPNLNNLTAVGCSLALAAVFPLGLDGYHIGRNQFPFV
CQARLWLLGLGFSLGYGSMFTKIWWVHTVFTKKEEKKEWRKTLEPWKLY
ATVGLLVGMDVLTLAIWQIVDPLHRTIETFAKEEPKEDIDVSILPQLEHCSS
RKMNTWLGIFYGYKGLLLLLGIFLAYETKSVSTEKINDHRAVGMAIYNVA
VLCLITAPVTMILSSQQDAAFAFASLAIVFSSYITLVVLFVPKMRRLITRGE
WQSEAQDTMKTGSSTNNNEEEKSRLLEKENRELEKIIAEKEERVSELRHQLQ
SRQQLRSRRHPPTPPEPSGGLPRGPPEPPDRLSCDGSRVHLLYK

FIG.18A

```
   1 atgttgctgc tgctgctact ggcgccactc ttcctccgcc ccccgggcgc gggcggggcg
  61 catacccccа acgccacctc agaaggttgc cagatcatac acccgccctg ggaagggggc
 121 atcaggtacc ggggcctgac tcgggaccag gtgaaggcta tcaacttcct gccagtggac
 181 tatgagattg agtatgtgtg ccgggggggag cgcgaggtgg tggggcccaa ggtccgcaag
 241 tgcctggcca acggctcctg gacagatatg gacacaccca gccgctgtgt ccgaatctgc
 301 tccaagtctt atttgaccct ggaaaatggg aaggttttcc tgacgggtgg ggacctccca
 361 gctctggacg gagcccgggc ggatttccgg tgtgaccccg acttccatct ggtgggcagc
 421 tcccggagca tctgtagtca gggccagtgg agcaccccca agccccactg ccaggtgaat
 481 cgaacgccac actcagaacg gcgcgcagtg tacatcgggg cactgtttcc catgagcggg
 541 ggctggccag ggggccaggc ctgccagccc gcggtggaga tggcgctgga ggacgtgaat
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 661 gatccaggcc aagccaccaa gtacctatat gagctgctct acaacgaccc tatcaagatc
 721 atccttatgc ctggctgcag ctctgtctcc acgctggtgg ctgaggctgc taggatgtgg
 781 aacctcattg tgctttccta tggctccagc tcaccagccc tgtcaaaccg gcagcgtttc
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 961 tcgactctgg acgacctgga ggaacgagtg aaggaggctg gaattgagat tactttccgc
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2761 cagctccgct cccggcgcca cccaccgaca cccccagaac cctctggggg cctgcccagg
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2881 aagtga
```

FIG.18B

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 121 aggtaccggg gcctgactcg ggaccaggtg aaggctatca acttcctgcc agtggactat
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 301 aagtcttatt tgaccctgga aaatgggaag gttttcctga cgggtgggga cctcccagct
 361 ctggacggag cccgggtgga tttccggtgt gaccccgact tccatctggt gggcagctcc
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3061 tgggaaacag acctttttct ctcttactgc ttcatgtaat tttgtatcac ctcttcacaa
```

FIG.19A

```
3121  tttagttcgt acctggcttg aagctgctca ctgctcacac gctgcctcct cagcagcctc
3181  actgcatctt tctcttccca tgcaacaccc tcttctagtt accacggcaa cccctgcagc
3241  tcctctgcct ttgtgctctg ttcctgtcca gcaggggtct cccaacaagt gctctttcca
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3661  tagcatgctg agtcatgtct ttcctatttg cacacgtcca tgtttatcca tgtactttcc
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3961  ctccctttg ttttgtgttt ttttgagggg aattaaggaa aaataagtgg gggcaggttt
4021  ggagagctgc ttccagtgga tagttgatga gaatcctgac caaaggaagg cacccttgac
4081  tgttgggata gacagatgga cctatggggt gggaggtggt gtcccttca cactgtggtg
4141  tctcttgggg aaggatctcc ccgaatctca ataaaccagt gaacagtgtg actcggaaaa
4201  aaaaaaaaaa aaaaaaaaaa
```

FIG.19B

PROXIMAL TO HSN-1. FCMD, DYS LOCI ON CHROMOSOME 9

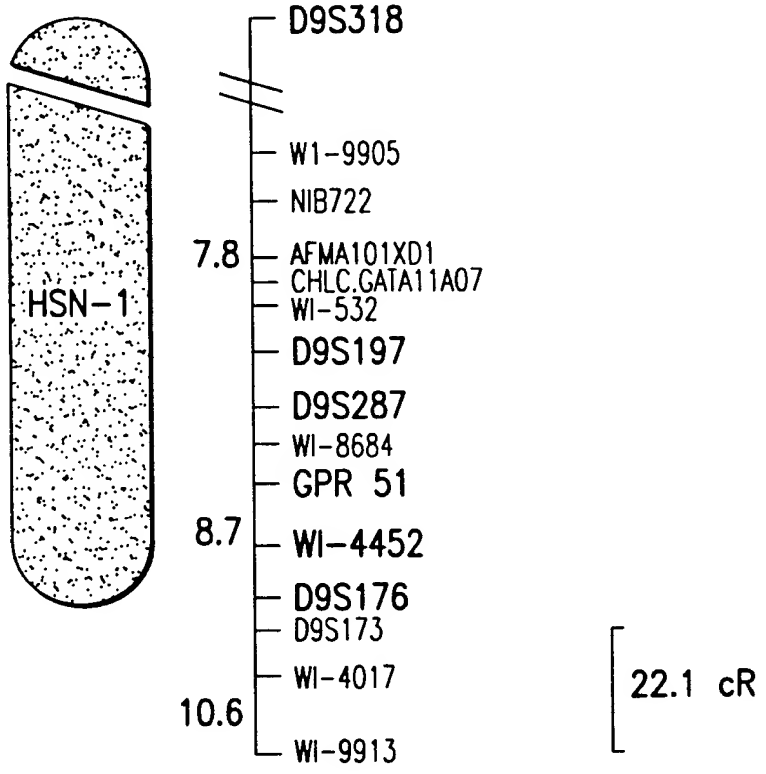

FIG. 20

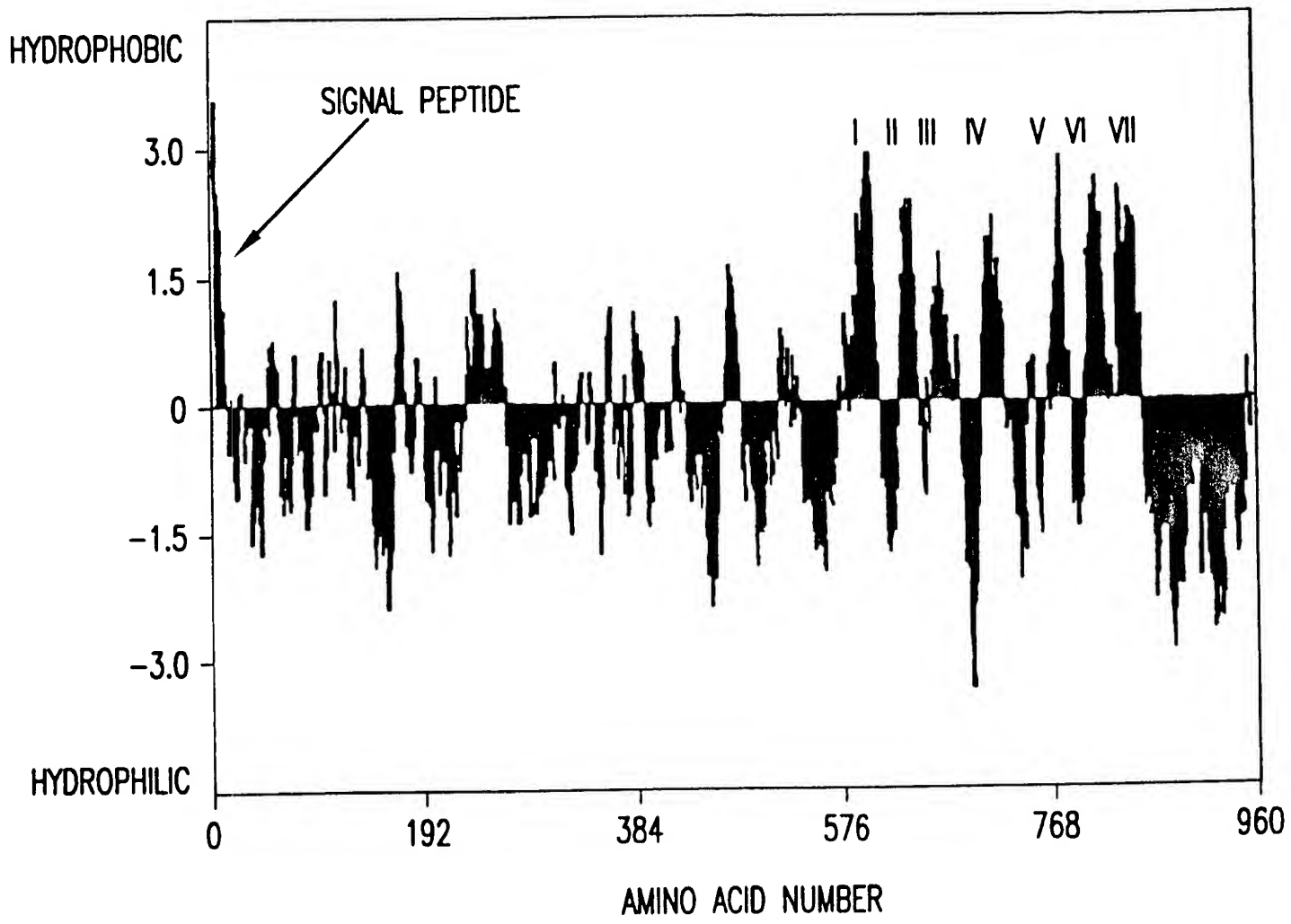

FIG.21

APPROVED BY DRAFTSMAN	O.G. FIG. CLASS	SUBCLASS

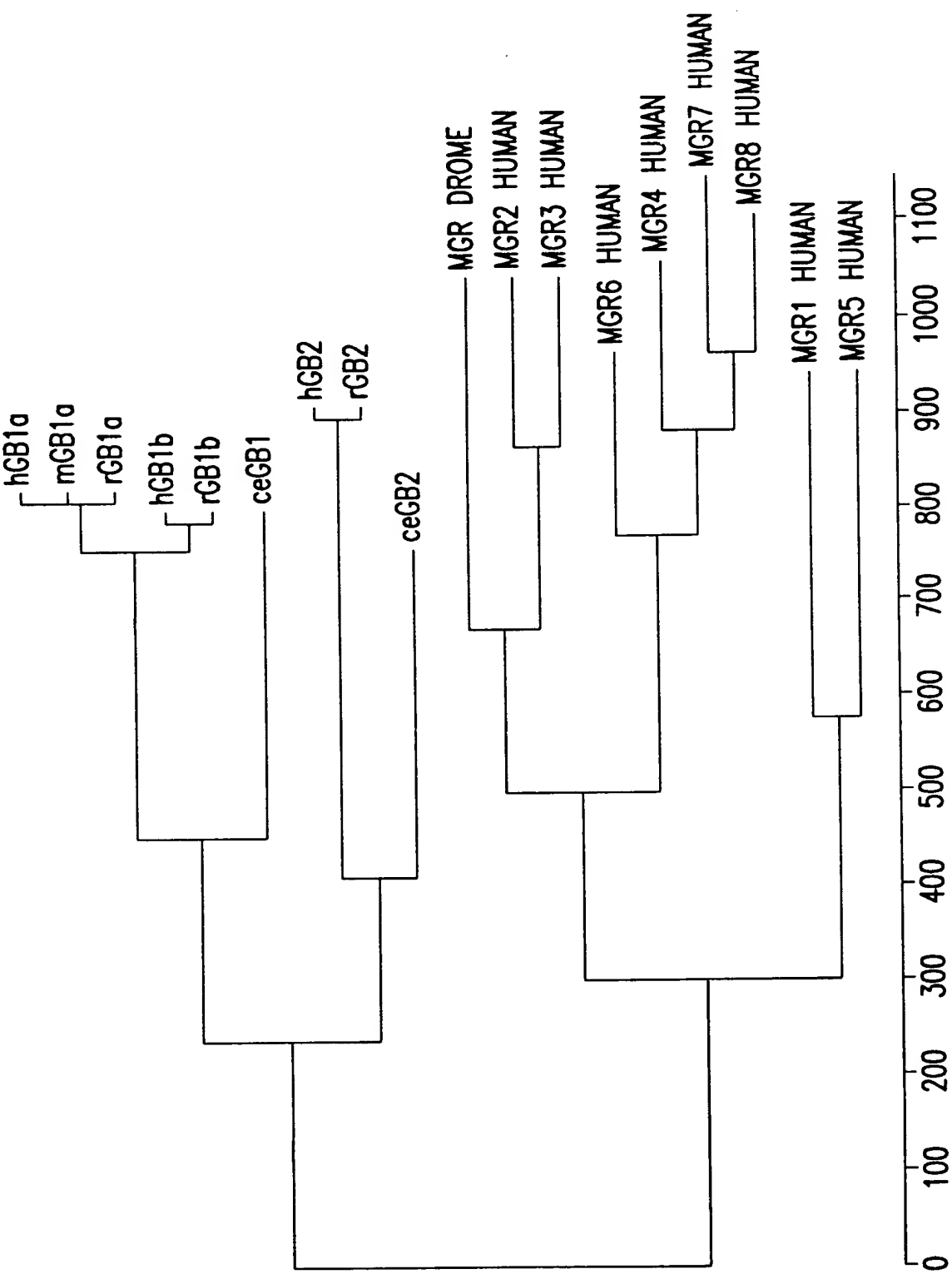

FIG. 22

COILED-COIL DOMAIN IN C-TERMINUS OF gb1a AND HG20
MEDIATING HETERODIMERIZATION

```
gb1   ....WQSEA.QDTMKTGSSTNNNEEEK...SRLLEK..ENRELEKIIAEKEERVSELRHQLQSRQQLRSRRHPP
hg20 QNRRFQFTQNQKKEDSKTSTSVTSVNQASTSRLEGLQSENHRLRMKITELDKDLEEVTMQLQDTPEKTTYIKQN
```

FIG.23

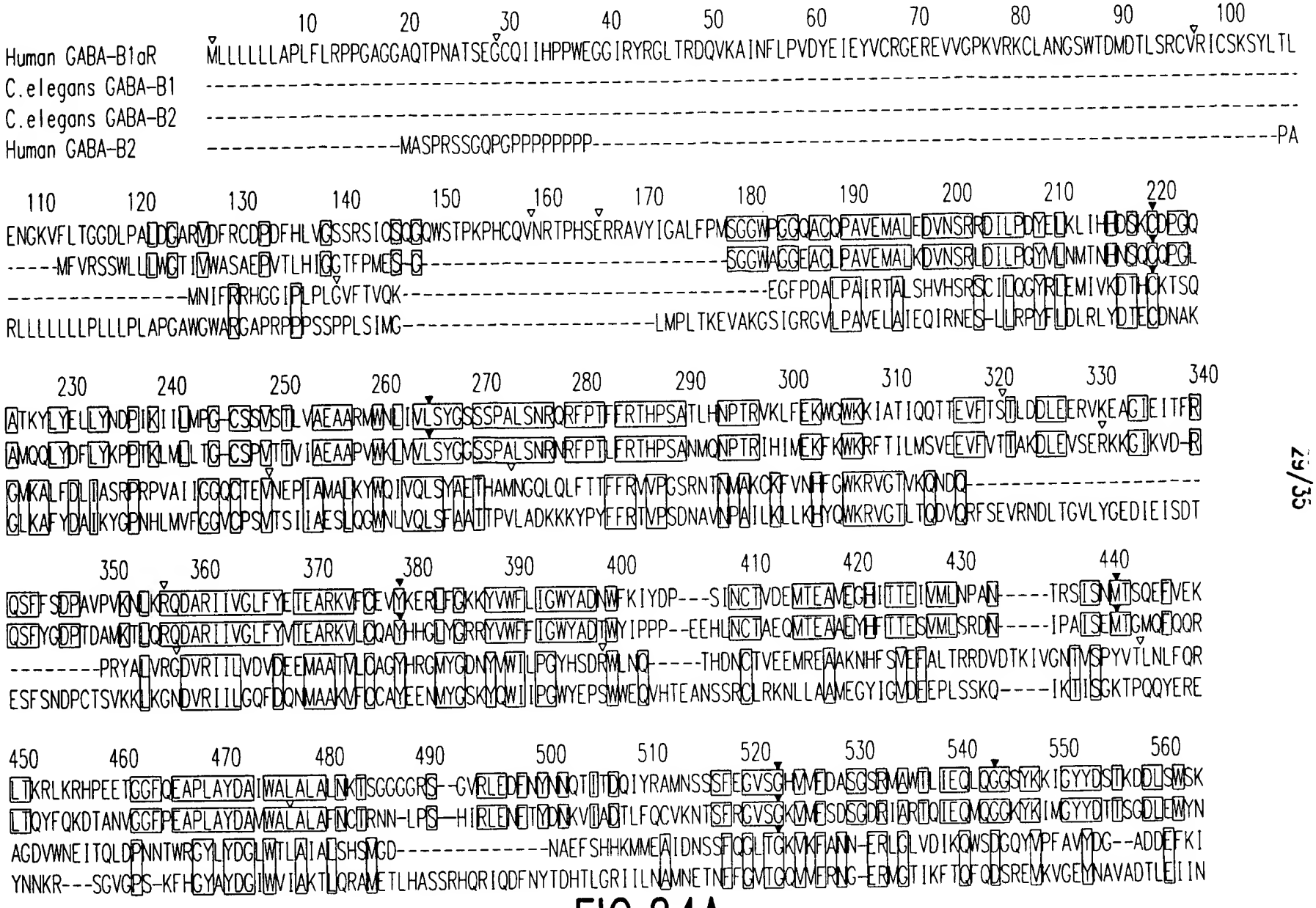

FIG.24A

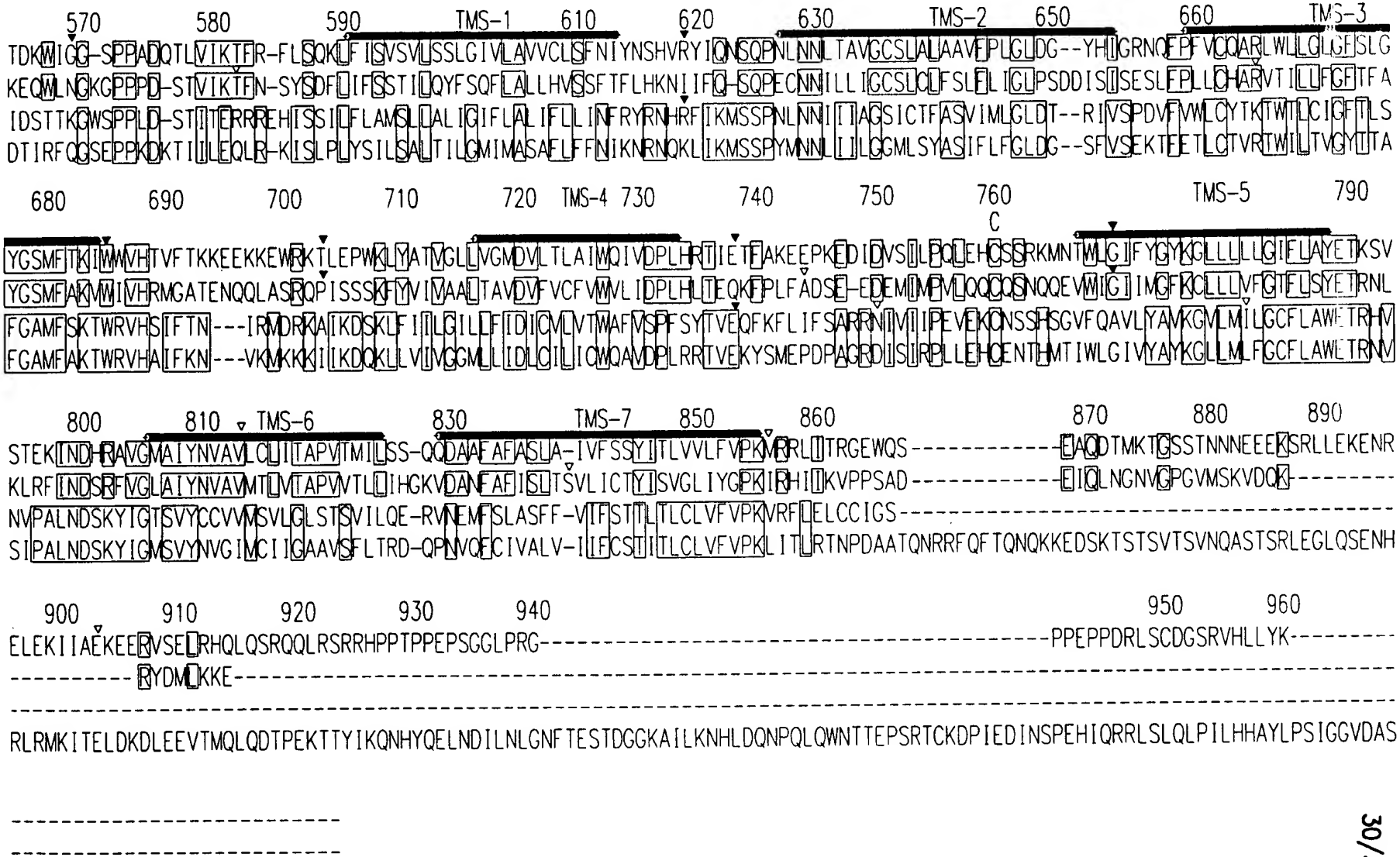

FIG.24B

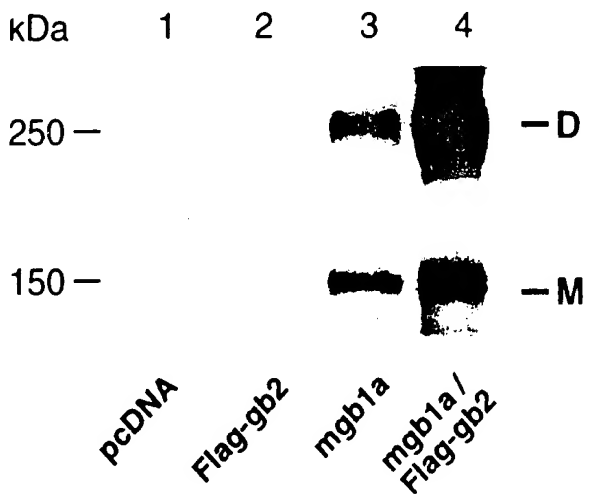

FIG.25A

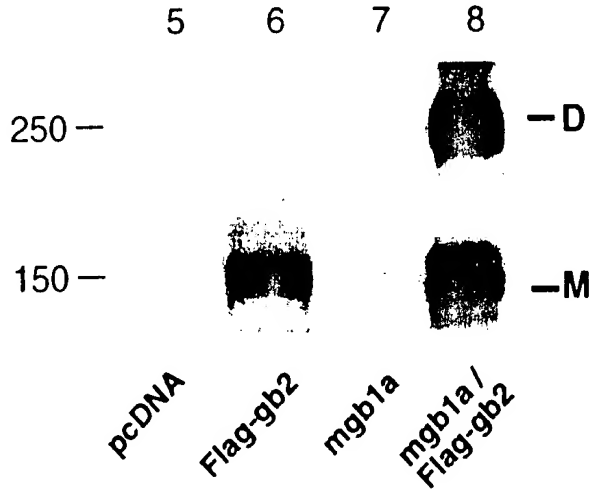

FIG.25B

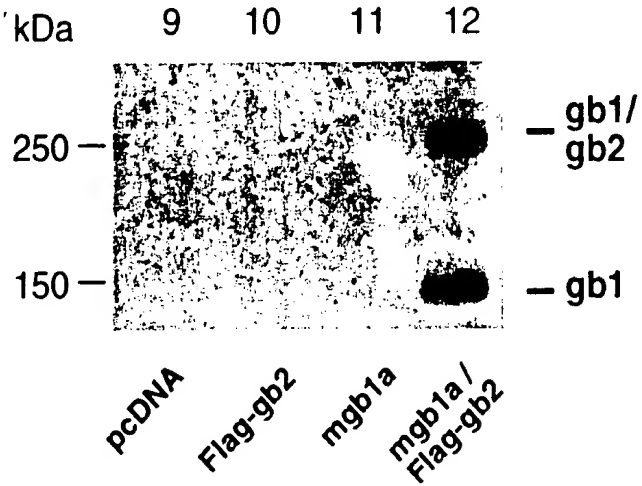

FIG.25C

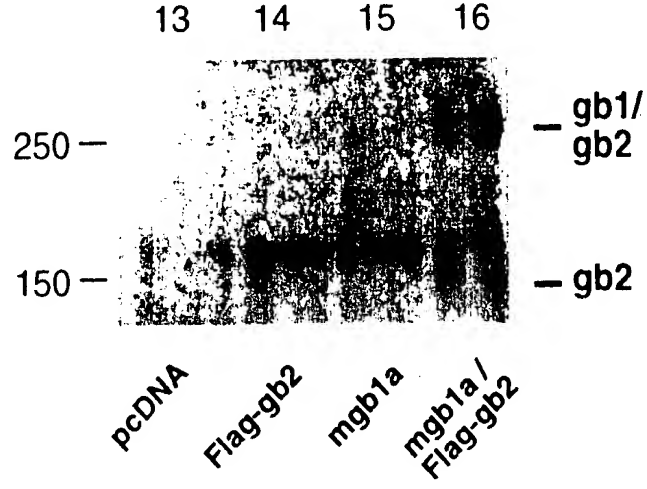

FIG.25D

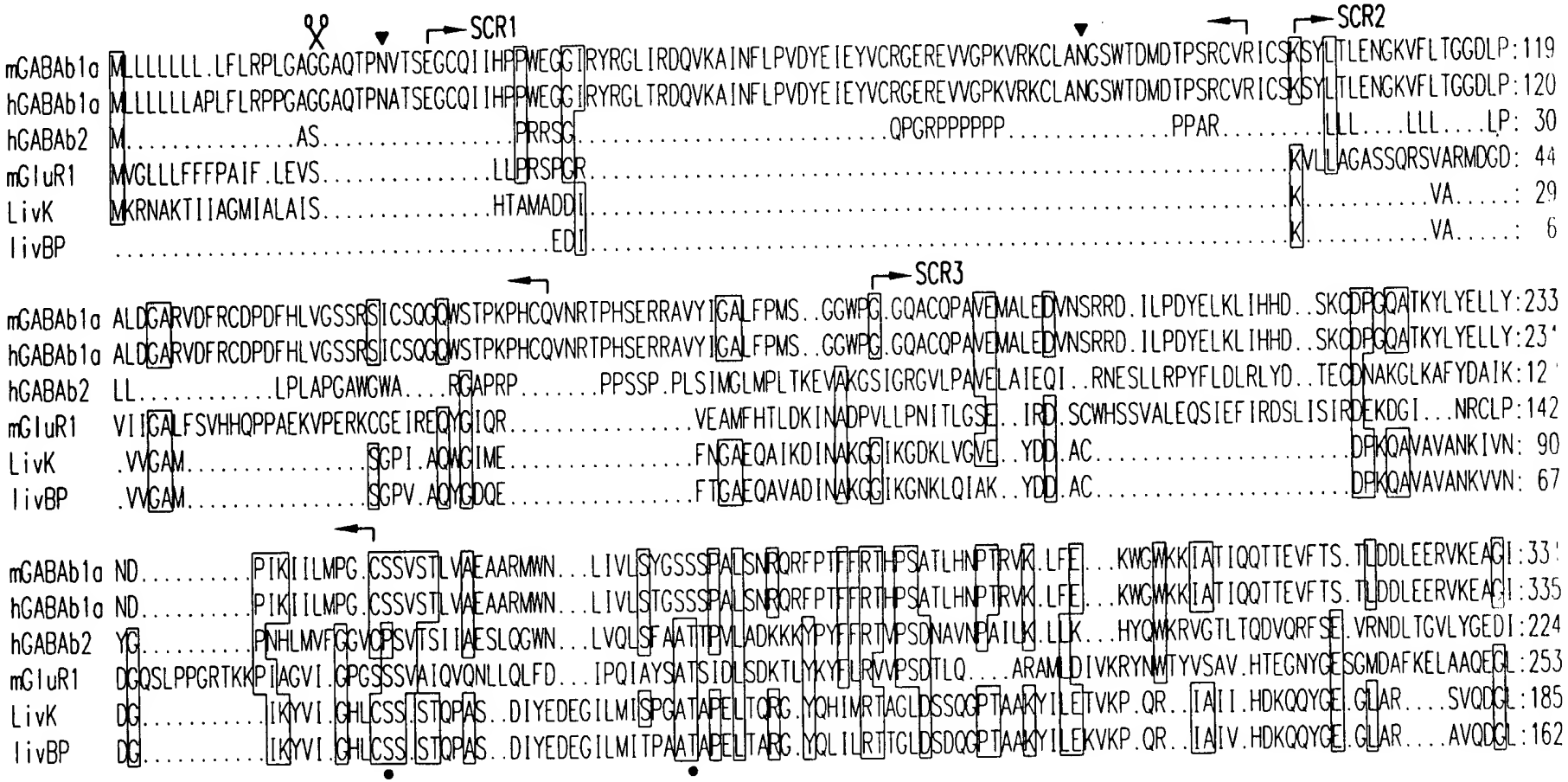

FIG.26A-1

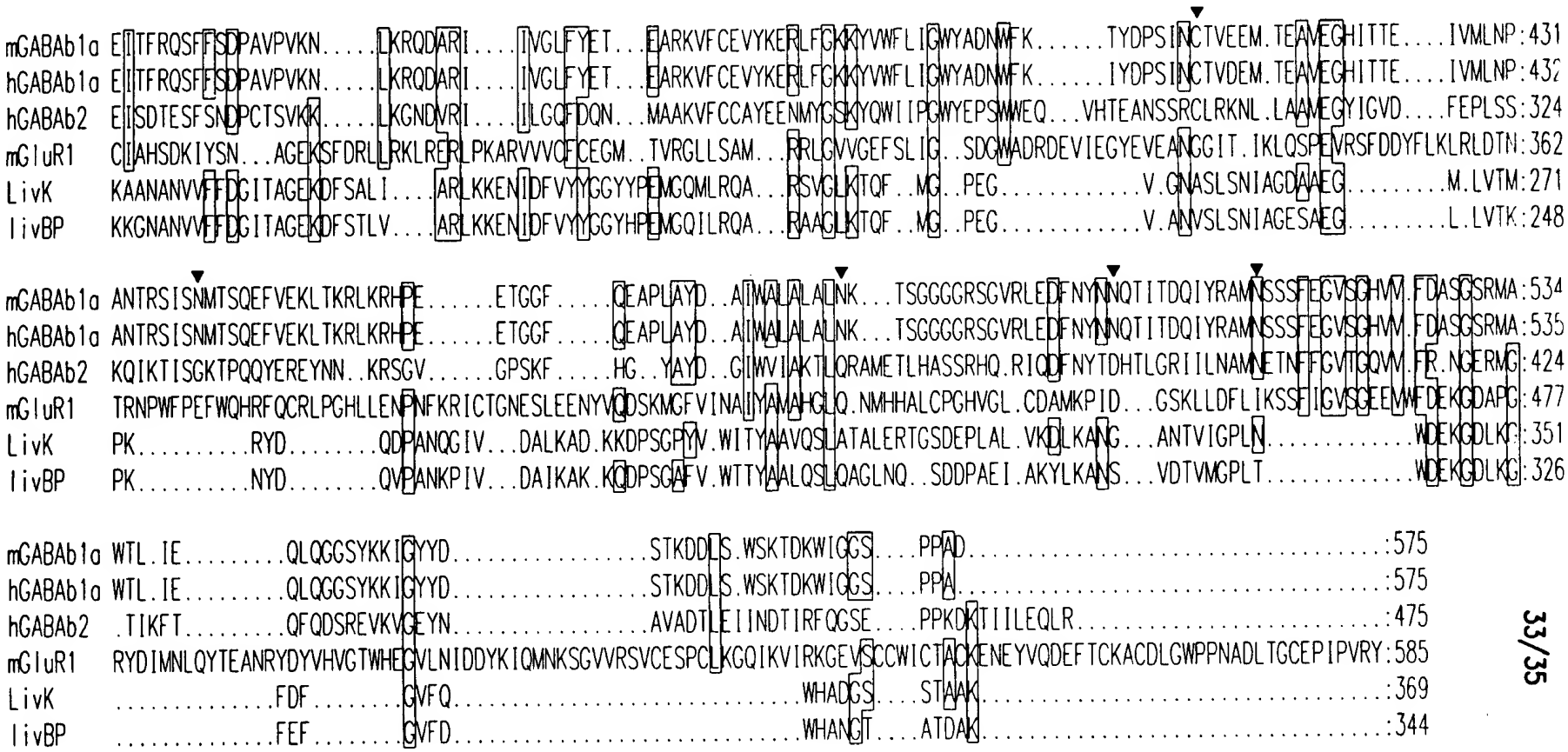

FIG.26A-2

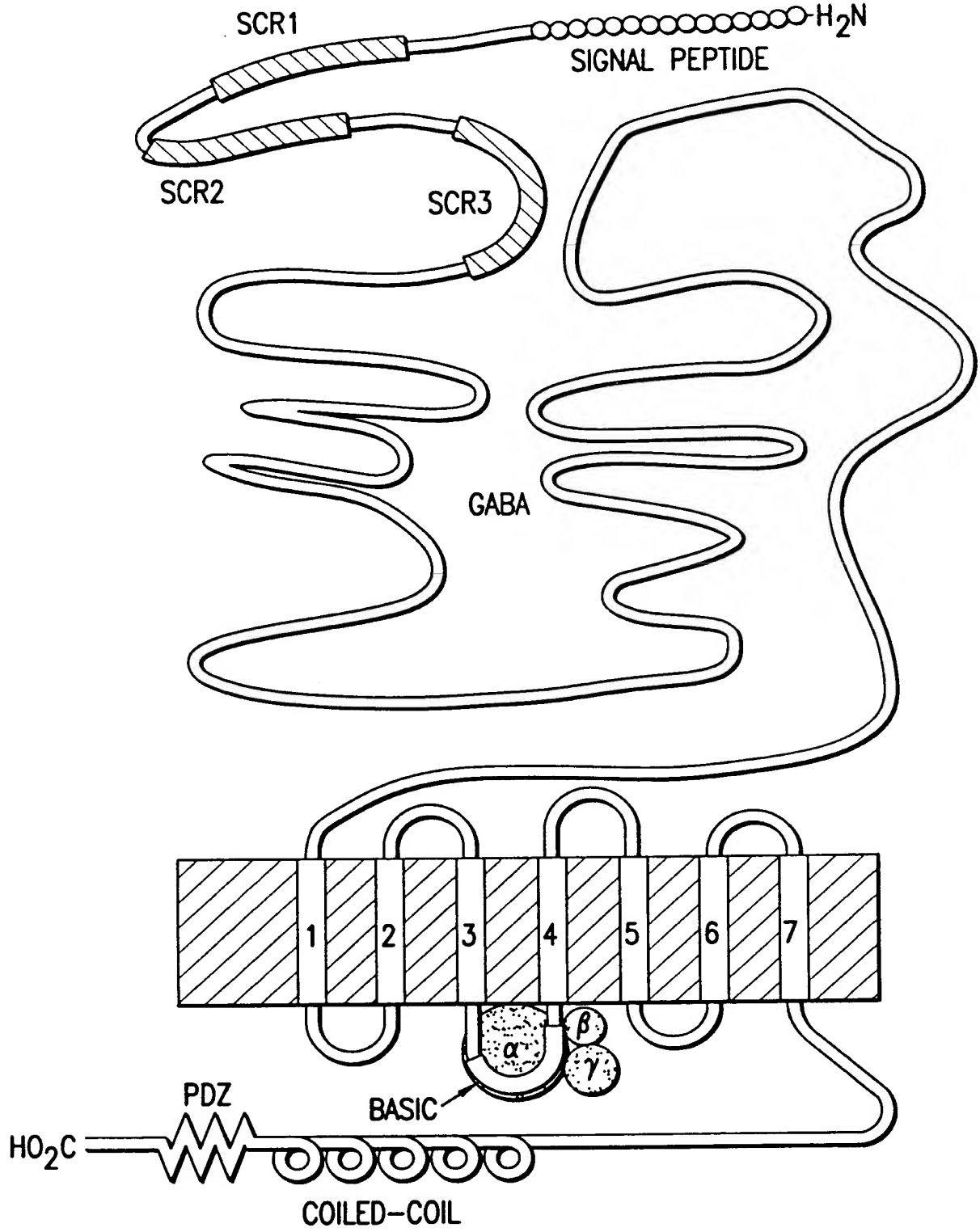

FIG.26B

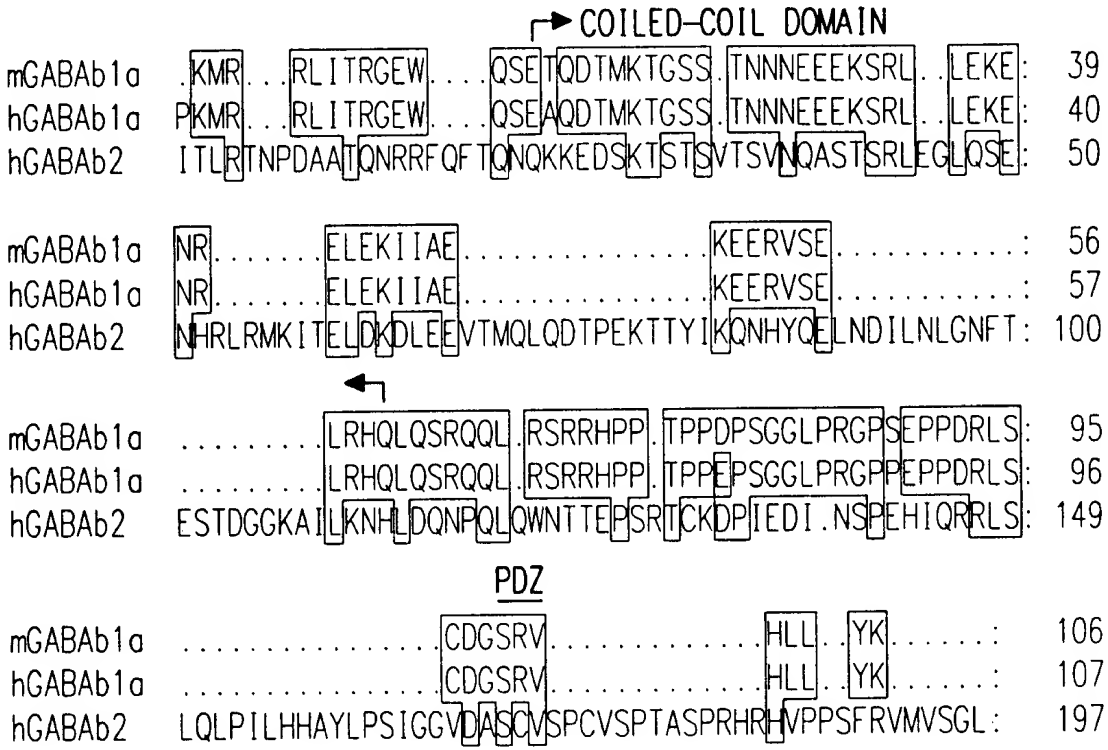

FIG.27